

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Fukudome, Kenji
Esmon, Charles T.

(ii) TITLE OF INVENTION: Cloning and Regulation of an Endothelial Cell Protein C/Activated Protein C Receptor

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Patrea L. Pabst
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/289,699
(B) FILING DATE: 12-AUG-1994
(C) CLASSIFICATION: 530

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pabst, Patrea L.
(B) REGISTRATION NUMBER: 31,284
(C) REFERENCE/DOCKET NUMBER: OMRF152

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1302
- (D) OTHER INFORMATION: /note= "Nucleotides 25 through 738 encode the

Endothelial Cell Protein Receptor of Sequence ID No. 2."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGGTCCGGA	GCCTCAACTT	CAGGATGTTG	ACAACATTGC	TGCCGATACT	GCTGCTGTCT	60
GGCTGGGCCT	TTTGTAGCCA	AGACGCCTCA	GATGCCCTCC	AAAGACTTCA	TATGCTCCAG	120
ATCTCCTACT	TCCGCGACCC	CTATCACGTG	TGGTACCAGG	GCAACCGCGTC	GCTGGGGGA	180
CACCTAACGC	ACGTGCTGGA	AGGCCAGAC	ACCAACACCA	CGATCATTCA	GCTGCAGCCC	240
TTGCAGGAGC	CCGAGAGCTG	GGCGCGCACG	CAGAGTGGCC	TGCAGTCCTA	CCTGCTCCAG	300
TTCCACGGCC	TCGTGCGCCT	GGTGCACCAAG	GAGCGGACCT	TGGCCTTTCC	TCTGACCATC	360
CGCTGCTTCC	TGGGCTGTGA	GCTGCCTCCC	GAGGGCTCTA	GAGCCCATGT	CTTCTTCGAA	420
GTGGCTGTGA	ATGGGAGCTC	CTTTGTGAGT	TTCCGGCCGG	AGAGAGCCTT	GTGGCAGGCA	480
GACACCCAGG	TCACCTCCGG	AGTGGTCACC	TTCACCCCTGC	AGCAGCTCAA	TGCCTACAAC	540
CGCACTCGGT	ATGAACTGCG	GGAATTCCCTG	GAGGACACCT	GTGTGCAGTA	TGTGCAGAAA	600
CATATTCGG	CGGAAAACAC	GAAAGGGAGC	CAAACAAGCC	GCTCCTACAC	TTCGCTGGTC	660
CTGGGCGTCC	TGGTGGCGG	TTTCATCATT	GCTGGTGTGG	CTGTAGGCAT	CTTCCTGTGC	720
ACAGGTGGAC	GGCGATGTTA	ATTACTCTCC	AGCCCCGTCA	GAAGGGGCTG	GATTGATGGA	780
GGCTGGCAAG	GGAAAGTTTC	AGCTCACTGT	GAAGCCAGAC	TCCCCAACTG	AAACACCAGA	840
AGGTTGGAG	TGACAGCTCC	TTTCTCTCC	CACATCTGCC	CACTGAAGAT	TTGAGGGAGG	900
GGAGATGGAG	AGGAGAGGTG	GACAAAGTAC	TTGGTTTGCT	AAGAACCTAA	GAACGTGTAT	960
GCTTGCTGA	ATTAGTCTGA	TAAGTGAATG	TTTATCTATC	TTTGTGGAAA	ACAGATAATG	1020
GAGTTGGGGC	AGGAAGCCTA	TGCGCCATCC	TCCAAAGACA	GACAGAATCA	CCTGAGGCCT	1080
TCAAAAGATA	TAACCAAATA	AAACAAGTCAT	CCACAATCAA	AATACAACAT	TCAATACTTC	1140
CAGGTGTGTC	AGACTTGGGA	TGGGACGCTG	ATATAATAGG	GTAGAAAGAA	GTAACACGAA	1200
GAAGTGGTGG	AAATGTAAAA	TCCAAGTCAT	ATGGCAGTGA	TCAATTATTA	ATCAATTAAT	1260
AATATTAATA	AATTCTTAT	ATTTAAAAAA	AAAAAA	AA		1302

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..365

(D) OTHER INFORMATION: /note= "Endothelial Cell Protein Receptor
encoded by
nucleotides 1 through 1302 of Sequence ID No. 1."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1..15

(D) OTHER INFORMATION: /note= "Amino acids 1-15 represent
a putative signal sequence."

(ix) FEATURE:

(A) NAME/KEY: Domain

(B) LOCATION: 211..236

(D) OTHER INFORMATION: /note= "Amino acids 211-236
represent a putative transmembrane domain."

(ix) FEATURE:

(A) NAME/KEY: Active-site

(B) LOCATION: 47..174

(D) OTHER INFORMATION: /note= "Amino acids 47-49, 64-66,
136-138 and 172-174 represent potential
N-glycosylation sites."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 17..186

(D) OTHER INFORMATION: /note= "Amino acids 17, 114, 118
and 186 represent extracellular cysteine
residues."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Thr Thr Leu Leu Pro Ile Leu Leu Ser Gly Trp Ala Phe
1 5 10 15

Cys Ser Gln Asp Ala Ser Asp Gly Leu Gln Arg Leu His Met Leu Gln
20 25 30

Ile Ser Tyr Phe Arg Asp Pro Tyr His Val Trp Tyr Gln Gly Asn Ala
35 40 45

Ser Leu Gly Gly His Leu Thr His Val Leu Glu Gly Pro Asp Thr Asn
50 55 60

Thr Thr Ile Ile Gln Leu Gln Pro Leu Gln Glu Pro Glu Ser Trp Ala
65 70 75 80

Arg Thr Gln Ser Gly Leu Gln Ser Tyr Leu Leu Gln Phe His Gly Leu
85 90 95

Val Arg Leu Val His Gln Glu Arg Thr Leu Ala Phe Pro Leu Thr Ile
100 105 110

Arg Cys Phe Leu Gly Cys Glu Leu Pro Pro Glu Gly Ser Arg Ala His
115 120 125

Val Phe Phe Glu Val Ala Val Asn Gly Ser Ser Phe Val Ser Phe Arg
130 135 140

Pro Glu Arg Ala Leu Trp Gln Ala Asp Thr Gln Val Thr Ser Gly Val
145 150 155 160

Val Thr Phe Thr Leu Gln Gln Leu Asn Ala Tyr Asn Arg Thr Arg Tyr
165 170 175

Glu Leu Arg Glu Phe Leu Glu Asp Thr Cys Val Gln Tyr Val Gln Lys
180 185 190

His Ile Ser Ala Glu Asn Thr Lys Gly Ser Gln Thr Ser Arg Ser Tyr
195 200 205

Thr Ser Leu Val Leu Gly Val Leu Val Gly Gly Phe Ile Ile Ala Gly
210 215 220

Val Ala Val Gly Ile Phe Leu Cys Thr Gly Gly Arg Arg Cys
225 230 235

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Leu Thr Lys Phe Leu Leu Leu Leu Leu Leu Pro Gly Cys
1 5 10 15

Ala Phe Val Thr Pro Met Ala Pro Lys Ala Ala Tyr Ala Pro Asp Leu
20 25 30

Leu Phe Pro Arg Pro Pro Ser Cys Glu Ala Ser Gly Gln Arg Ser Leu
35 40 45

Gly Lys Leu Leu Thr His Thr Leu Glu Gly Pro Ser Gln Asn Val Thr
50 55 60

Ile Leu Gln Leu Gln Pro Trp Gln Asp Pro Glu Ser Trp Glu Arg Thr
65 70 75 80

Glu Ser Gly Leu Gln Ile Tyr Leu Thr Gln Phe Glu Ser Leu Val Lys
85 90 95

Leu Val Tyr Arg Glu Arg Lys Glu Asn Val Phe Phe Pro Leu Thr Val
100 105 110

Ser Cys Ser Leu Gly Cys Glu Leu Pro Glu Glu Glu Gly Ser
115 120 125

Glu Pro His Val Phe Phe Asp Val Ala Val Asn Gly Ser Ala Phe Val
130 135 140

Ser Phe Arg Pro Lys Thr Ala Val Trp Val Ser Gly Ser Gln Glu Pro
145 150 155 160

Ser Lys Ala Ala Asn Phe Thr Leu Lys Gln Leu Asn Ala Tyr Asn Arg
165 170 175

Thr Arg Tyr Glu Leu Gln Glu Phe Leu Gln Asp Thr Cys Val Glu Phe
180 185 190

Leu Glu Asn His Ile Thr Thr Gln Asn Met Lys Gly Ser Gln Thr Gly
195 200 205

Arg Ser Tyr Thr Ser Leu Val Leu Gly Ile Leu Met Gly Cys Phe Ile
210 215 220

Ile Ala Gly Val Ala Val Gly Ile Phe Met Cys Thr Ser Gly Arg Gly
225 230 235 240

Leu Leu Ile Ile

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
1 5 10 15

Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
20 25 30

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala
35 40 45

Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp Thr

50	55	60
Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln		
65	70	75
Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr		
85	90	95
Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu		
100	105	110
Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Ser		
115	120	125
Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe		
130	135	140
Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn		
145	150	155
Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr Val		
165	170	175
Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu		
180	185	190
Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp		
195	200	205
Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val Cys		
210	215	220
His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Arg		
225	230	235
Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn		
245	250	255
Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly		
260	265	270
Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly		
275	280	285
Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu		
290	295	300
Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly		
305	310	315
Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu		
325	330	335

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Arg Tyr Leu Pro Cys Leu Leu Leu Trp Ala Phe Leu Gln Val Trp
1 5 10 15

Gly Gln Ser Glu Val Gln Gln Lys Asn Tyr Thr Phe Arg Cys Leu Gln
20 25 30

Thr Ser Ser Phe Ala Asn Ile Ser Trp Ser Arg Thr Asp Ser Leu Ile
35 40 45

Leu Leu Gly Asp Leu Gln Thr His Arg Trp Ser Asn Asp Ser Ala Thr
50 55 60

Ile Ser Phe Thr Lys Pro Trp Ser Gln Gly Lys Leu Ser Asn Gln Gln
65 70 80

Trp Glu Lys Leu Gln His Met Phe Gln Val Tyr Arg Val Ser Phe Thr
85 90 95

Arg Asp Ile Gln Glu Leu Val Lys Met Met Ser Pro Lys Glu Asp Tyr
100 105 110

Pro Ile Glu Ile Gln Leu Ser Thr Gly Cys Glu Met Tyr Pro Gly Asn
115 120 125

Ala Ser Glu Ser Phe Phe His Val Ala Phe Gln Gly Lys Tyr Ala Val
130 135 140

Arg Phe Arg Gly Thr Ser Trp Gln Arg Val Leu Gly Ala Pro Ser Trp
145 150 160

Leu Asp Leu Pro Ile Lys Val Leu Asn Ala Asp Gln Gly Thr Ser Ala
165 170 175

Thr Val Gln Thr Leu Leu Asn Asp Thr Trp Pro Gln Phe Ala Arg Gly
180 185 190

Leu Leu Glu Ala Gly Lys Ser Asp Leu Glu Lys Gln Glu Lys Pro Val
195 200 205

Ala Trp Leu Ser Ser Val Pro Ser Ser Ala His Gly His Leu Gln Leu
210 215 220

Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Met Trp
225 230 240

Met Arg Gly Asp Gln Glu Gln Gln Gly Thr His Arg Gly Asp Phe Leu

245

250

255

Pro Asn Ala Asp Glu Thr Trp Tyr Leu Gln Ala Thr Leu Asp Val Glu
260 265 270

Ala Gly Glu Glu Ala Gly Leu Ala Cys Arg Val Lys His Ser Ser Leu
275 280 285

Gly Gly Gln Asp Ile Ile Leu Tyr Trp Asp Ala Arg Gln Ala Pro Val
290 295 300

Gly Leu Ile Val Phe Ile Val Leu Ile Met Leu Val Val Val Gly Ala
305 310 315 320

Val Val Tyr Tyr Ile Trp Arg Arg Arg Ser Ala Tyr Gln Asp Ile Arg
325 330 335

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Thr Lys Phe Leu Pro Leu Leu Leu Leu Leu Pro Gly Cys
1 5 10 15

Ala Leu Cys Asn Ser Asp Gly Ser Gln Ser Leu His Met Leu Gln Ile
20 25 30

Ser Tyr Phe Gln Asp His His His Val Arg His Gln Gly Asn Ala Ser
35 40 45

Leu Gly Lys Leu Leu Thr His Thr Leu Glu Gly Pro Ser Gln Asn Val
50 55 60

Thr Ile Leu Gln Leu Gln Pro Trp Gln Asp Pro Glu Ser Trp Glu Arg
65 70 75 80

Thr Glu Ser Gly Leu Gln Ile Tyr Leu Thr Gln Phe Glu Ser Leu Val
85 90 95

Lys Leu Val Tyr Arg Glu Arg Lys Glu Asn Val Phe Phe Pro Leu Thr
100 105 110

Val Ser Cys Ser Leu Gly Cys Glu Leu Pro Glu Glu Glu Gly
115 120 125

Ser Glu Pro His Val Phe Phe Asp Val Ala Val Asn Gly Ser Ala Phe

130

135

140

Val Ser Phe Arg Pro Lys Thr Ala Val Trp Val Ser Gly Ser Gln Glu
145 150 155 160

Pro Ser Lys Ala Ala Asn Phe Thr Leu Lys Gln Leu Asn Ala Tyr Asn
165 170 175

Arg Thr Arg Tyr Glu Leu Gln Glu Phe Leu Gln Asp Thr Cys Val Glu
180 185 190

Phe Leu Glu Asn His Ile Thr Thr Gln Asn Met Lys Gly Ser Gln Thr
195 200 205

Gly Arg Ser Tyr Thr Ser Leu Val Leu Gly Ile Leu Met Gly Cys Phe
210 215 220

Ile Ile Ala Gly Val Ala Val Gly Ile Phe Met Cys Thr Ser Gly Arg
225 230 235 240

Arg Cys

C
Cont